

SEQUENCE LISTING

<110> Herrmann, Rafael
 Lu, Albert L.
 McCutchen, Billy Fred
 Presnail, James K.
 Wong, James F. H.

<120> Orally Active Pesticidal Biopeptides

<130> 35718/260673

<150> 60/395,428

<151> 2002-07-12

<160> 27

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 355

<212> DNA

<213> Centruroides vittatus

<220>

<221> CDS

<222> (49)...(303)

<221> misc_feature

<222> (0)...(0)

<223> CV1

<400> 1

ggatcccccg ggctgcagga gaatttatac gttatcagaa aactcaaa atg aat tat 57
 Met Asn Tyr
 1

ttt ata ttg att ttg gtt gca gct cta tta ata ttg gat gca aat tgt 105
 Phe Ile Leu Ile Leu Val Ala Ala Leu Leu Ile Leu Asp Ala Asn Cys
 5 10 15

aag aaa gac gga tat cca gtt gat gcg gag gaa tgt aga tat aat tgt 153
 Lys Lys Asp Gly Tyr Pro Val Asp Ala Glu Glu Cys Arg Tyr Asn Cys
 20 25 30 35

tgg aaa aac gaa tac tgc gac aaa atc tgc aaa gag aag aaa ggt gaa 201
 Trp Lys Asn Glu Tyr Cys Asp Lys Ile Cys Lys Glu Lys Lys Gly Glu
 40 45 50

agt gga tat tgt tac gga tgg aat ctg tcg tgt tgg tgt ata ggt ctt 249
 Ser Gly Tyr Cys Tyr Gly Trp Asn Leu Ser Cys Trp Cys Ile Gly Leu
 55 60 65

cct gat gat aca aat aca aaa atg aat ccc ttt tgt cag ggt ttg gat 297

Pro Asp Asp Thr Asn Thr Lys Met Asn Pro Phe Cys Gln Gly Leu Asp
70 75 80

ggg taa acgaaattta accaataaaaa aaaaaaaaaa ggggaaatct gctttttacta 353
Gly *

at 355

<210> 2
<211> 84
<212> PRT
<213> Centruroides vittatus

<400> 2
Met Asn Tyr Phe Ile Leu Ile Leu Val Ala Ala Leu Leu Ile Leu Asp
1 5 10 15
Ala Asn Cys Lys Lys Asp Gly Tyr Pro Val Asp Ala Glu Glu Cys Arg
20 25 30
Tyr Asn Cys Trp Lys Asn Glu Tyr Cys Asp Lys Ile Cys Lys Glu Lys
35 40 45
Lys Gly Glu Ser Gly Tyr Cys Tyr Gly Trp Asn Leu Ser Cys Trp Cys
50 55 60
Ile Gly Leu Pro Asp Asp Thr Asn Thr Lys Met Asn Pro Phe Cys Gln
65 70 75 80
Gly Leu Asp Gly

<210> 3
<211> 255
<212> DNA
<213> Centruroides vittatus

<220>
<221> CDS
<222> (1)...(255)

<400> 3
atg aat tat ttt ata ttg att ttg gtt gca gct cta tta ata ttg gat 48
Met Asn Tyr Phe Ile Leu Ile Leu Val Ala Ala Leu Leu Ile Leu Asp
1 5 10 15
gca aat tgt aag aaa gac gga tat cca gtt gat gcg gag gaa tgt aga 96
Ala Asn Cys Lys Lys Asp Gly Tyr Pro Val Asp Ala Glu Glu Cys Arg
20 25 30
tat aat tgt tgg aaa aac gaa tac tgc gac aaa atc tgc aaa gag aag 144
Tyr Asn Cys Trp Lys Asn Glu Tyr Cys Asp Lys Ile Cys Lys Glu Lys
35 40 45
aaa ggt gaa agt gga tat tgt tac gga tgg aat ctg tcg tgt tgg tgt 192
Lys Gly Glu Ser Gly Tyr Cys Tyr Gly Trp Asn Leu Ser Cys Trp Cys
50 55 60
ata ggt ctt cct gat gat aca aat aca aaa atg aat ccc ttt tgt cag 240
Ile Gly Leu Pro Asp Asp Thr Asn Thr Lys Met Asn Pro Phe Cys Gln

65	70	75	80	
ggt ttg gat ggg taa				255
Gly Leu Asp Gly *				

<210> 4
 <211> 64
 <212> PRT
 <213> Centruroides vittatus

<400> 4	
Lys Lys Asp Gly Tyr Pro Val Asp Ala Glu Glu Cys Arg Tyr Asn Cys	
1 5 10 15	
Trp Lys Asn Glu Tyr Cys Asp Lys Ile Cys Lys Glu Lys Lys Gly Glu	
20 25 30	
Ser Gly Tyr Cys Tyr Gly Trp Asn Leu Ser Cys Trp Cys Ile Gly Leu	
35 40 45	
Pro Asp Asp Thr Asn Thr Lys Met Asn Pro Phe Cys Gln Gly Leu Asp	
50 55 60	

<210> 5
 <211> 267
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Codon biased nucleotide sequence encoding CV1.
 Codon biased for rice.

<221> CDS
 <222> (73)...(267)

<221> sig_peptide
 <222> (1)...(72)
 <223> BAA signal peptide

<400> 5	
atg gcc aac aag cac ctc tcc ctg agc ctt ttc ttg gtg ctc cta ggc	48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly	
-20 -15 -10	
ctg tcg gcg tct tta gct tca ggg aag aaa gac ggc tac ccg gtg gat	96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Lys Asp Gly Tyr Pro Val Asp	
-5 1 5	
gcc gag gaa tgc cgc tat aac tgt tgg aag aat gag tac tgc gac aag	144
Ala Glu Glu Cys Arg Tyr Asn Cys Trp Lys Asn Glu Tyr Cys Asp Lys	
10 15 20	
atc tgc aag gag aaa aag ggg gaa tcc gga tac tgt tat ggc tgg aac	192
Ile Cys Lys Glu Lys Lys Gly Glu Ser Gly Tyr Cys Tyr Gly Trp Asn	
25 30 35 40	
ctc agc tgc tgg tgc att ggc ctg ccc gat gac acc aat acg aag atg	240

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Leu Ser Cys Trp Cys Ile Gly Leu Pro Asp Asp Thr Asn Thr Lys Met
          45                      50                      55

aac cca ttc tgc cag ggg ctt gat tga
Asn Pro Phe Cys Gln Gly Leu Asp  *
          60

<210> 6
<211> 375
<212> DNA
<213> Leiurus quinquestriatus

<220>
<221> CDS
<222> (38)...(298)

<221> misc_feature
<222> (0)...(0)
<223> LghIV

<221> misc_feature
<222> 18, 33, 374
<223> n = A,T,C or G

<400> 6
gaattcggca cctcgtgnaa tttcggcaca gtncaaa atg aat tac ttg atg ata 55
                      Met Asn Tyr Leu Met Ile
                      1                      5

att agt ttg gct ctt ctt cta atg aca ggt gtg gag agc ggt gta cgt 103
Ile Ser Leu Ala Leu Leu Leu Met Thr Gly Val Glu Ser Gly Val Arg
          10                      15                      20

gat gct tat att gcc gac gat aaa aac tgt gtg tac act tgt ggt gca 151
Asp Ala Tyr Ile Ala Asp Asp Lys Asn Cys Val Tyr Thr Cys Gly Ala
          25                      30                      35

aat tca tat tgc aac aca gaa tgt acc aag aac ggt gct gag agt ggc 199
Asn Ser Tyr Cys Asn Thr Glu Cys Thr Lys Asn Gly Ala Glu Ser Gly
          40                      45                      50

tat tgt caa tgg ttt ggt aaa tat gga aat gcc tgc tgg tgc ata aag 247
Tyr Cys Gln Trp Phe Gly Lys Tyr Gly Asn Ala Cys Trp Cys Ile Lys
          55                      60                      65                      70

ttg ccc gat aaa gta cct att aga ata cca gga aag tgc cgt ggc cga 295
Leu Pro Asp Lys Val Pro Ile Arg Ile Pro Gly Lys Cys Arg Gly Arg
          75                      80                      85

taa atttaagatg gaatataacc taaatataac tgttaaataa atataattta 348
*

aaaattttaa aaaaaaaaaa aaaaanc 375

<210> 7

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<211> 86
 <212> PRT
 <213> Leiurus quinquestriatus

<400> 7
 Met Asn Tyr Leu Met Ile Ile Ser Leu Ala Leu Leu Leu Met Thr Gly
 1 5 10 15
 Val Glu Ser Gly Val Arg Asp Ala Tyr Ile Ala Asp Asp Lys Asn Cys
 20 25 30
 Val Tyr Thr Cys Gly Ala Asn Ser Tyr Cys Asn Thr Glu Cys Thr Lys
 35 40 45
 Asn Gly Ala Glu Ser Gly Tyr Cys Gln Trp Phe Gly Lys Tyr Gly Asn
 50 55 60
 Ala Cys Trp Cys Ile Lys Leu Pro Asp Lys Val Pro Ile Arg Ile Pro
 65 70 75 80
 Gly Lys Cys Arg Gly Arg
 85

<210> 8
 <211> 261
 <212> DNA
 <213> Leiurus quinquestriatus

<220>
 <221> CDS
 <222> (1)...(261)

<221> misc_feature
 <222> (0)...(0)
 <223> LghIV

<400> 8
 atg aat tac ttg atg ata att agt ttg gct ctt ctt cta atg aca ggt 48
 Met Asn Tyr Leu Met Ile Ile Ser Leu Ala Leu Leu Leu Met Thr Gly
 1 5 10 15
 gtg gag agc ggt gta cgt gat gct tat att gcc gac gat aaa aac tgt 96
 Val Glu Ser Gly Val Arg Asp Ala Tyr Ile Ala Asp Asp Lys Asn Cys
 20 25 30
 gtg tac act tgt ggt gca aat tca tat tgc aac aca gaa tgt acc aag 144
 Val Tyr Thr Cys Gly Ala Asn Ser Tyr Cys Asn Thr Glu Cys Thr Lys
 35 40 45
 aac ggt gct gag agt ggc tat tgt caa tgg ttt ggt aaa tat gga aat 192
 Asn Gly Ala Glu Ser Gly Tyr Cys Gln Trp Phe Gly Lys Tyr Gly Asn
 50 55 60
 gcc tgc tgg tgc ata aag ttg ccc gat aaa gta cct att aga ata cca 240
 Ala Cys Trp Cys Ile Lys Leu Pro Asp Lys Val Pro Ile Arg Ile Pro
 65 70 75 80
 gga aag tgc cgt ggc cga taa 261
 Gly Lys Cys Arg Gly Arg *
 85

<210> 9
 <211> 483
 <212> DNA
 <213> *Vaejovis carolinanus*

<220>
 <221> CDS
 <222> (65)...(358)

<221> misc_feature
 <222> (0)...(0)
 <223> VC1

<400> 9
 gccgctctag aactagtgga tcccccgggc tgcaggtttc tccgtttgga taatcgtcta 60
 gaaa atg aac gct aaa ata act gtt cta ttt ttc ctc gta gcc att aca 109
 Met Asn Ala Lys Ile Thr Val Leu Phe Phe Leu Val Ala Ile Thr
 1 5 10 15
 att gct tct tgt gcc tgg ata agt gag aaa aaa gtt caa gat gtc att 157
 Ile Ala Ser Cys Ala Trp Ile Ser Glu Lys Lys Val Gln Asp Val Ile
 20 25 30
 gat aaa aaa ttg cca aac gga atg gtg aag aat gca atc aaa gcc gta 205
 Asp Lys Lys Leu Pro Asn Gly Met Val Lys Asn Ala Ile Lys Ala Val
 35 40 45
 gta cac aaa gca gcg aag aat aag cac ggc tgt ttt gct gat ttt gat 253
 Val His Lys Ala Ala Lys Asn Lys His Gly Cys Phe Ala Asp Phe Asp
 50 55 60
 gta gga gga gga tgc gaa cag cac tgc cag aaa acg gaa agt aaa gca 301
 Val Gly Gly Gly Cys Glu Gln His Cys Gln Lys Thr Glu Ser Lys Ala
 65 70 75
 gga atc tgt cac gga acc aaa tgc aaa tgc ggt att ccc cgt gcc tat 349
 Gly Ile Cys His Gly Thr Lys Cys Lys Cys Gly Ile Pro Arg Ala Tyr
 80 85 90 95
 aaa aaa taa atcactgatt aatgctaacg gtgaatacat ataatatattc 398
 Lys Lys *
 tatccaagct ttagtcaaaa ataataaaat gaattatttg cacacttaca ttctatgtaa 458
 tatacacaaa ataaatcgaa tttagg 483

<210> 10
 <211> 97
 <212> PRT
 <213> *Vaejovis carolinanus*

<400> 10
 Met Asn Ala Lys Ile Thr Val Leu Phe Phe Leu Val Ala Ile Thr Ile
 1 5 10 15
 Ala Ser Cys Ala Trp Ile Ser Glu Lys Lys Val Gln Asp Val Ile Asp
 20 25 30

Lys Lys Leu Pro Asn Gly Met Val Lys Asn Ala Ile Lys Ala Val Val
 35 40 45
 His Lys Ala Ala Lys Asn Lys His Gly Cys Phe Ala Asp Phe Asp Val
 50 55 60
 Gly Gly Gly Cys Glu Gln His Cys Gln Lys Thr Glu Ser Lys Ala Gly
 65 70 75 80
 Ile Cys His Gly Thr Lys Cys Lys Cys Gly Ile Pro Arg Ala Tyr Lys
 85 90 95
 Lys

<210> 11
 <211> 294
 <212> DNA
 <213> *Vaejovis carolinanus*

<220>
 <221> CDS
 <222> (1)...(294)
 <221> misc_feature
 <222> (0)...(0)
 <223> VC1

<400> 11
 atg aac gct aaa ata act gtt cta ttt ttc ctc gta gcc att aca att 48
 Met Asn Ala Lys Ile Thr Val Leu Phe Phe Leu Val Ala Ile Thr Ile
 1 5 10 15

 gct tct tgt gcc tgg ata agt gag aaa aaa gtt caa gat gtc att gat 96
 Ala Ser Cys Ala Trp Ile Ser Glu Lys Lys Val Gln Asp Val Ile Asp
 20 25 30

 aaa aaa ttg cca aac gga atg gtg aag aat gca atc aaa gcc gta gta 144
 Lys Lys Leu Pro Asn Gly Met Val Lys Asn Ala Ile Lys Ala Val Val
 35 40 45

 cac aaa gca gcg aag aat aag cac ggc tgt ttt gct gat ttt gat gta 192
 His Lys Ala Ala Lys Asn Lys His Gly Cys Phe Ala Asp Phe Asp Val
 50 55 60

 gga gga gga tgc gaa cag cac tgc cag aaa acg gaa agt aaa gca gga 240
 Gly Gly Gly Cys Glu Gln His Cys Gln Lys Thr Glu Ser Lys Ala Gly
 65 70 75 80

 atc tgt cac gga acc aaa tgc aaa tgc ggt att ccc cgt gcc tat aaa 288
 Ile Cys His Gly Thr Lys Cys Lys Cys Gly Ile Pro Arg Ala Tyr Lys
 85 90 95

 aaa taa 294
 Lys *

<210> 12
 <211> 312

<212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (76)...(312)

<221> sig_peptide
 <222> (1)...(75)
 <223> PR1 signal peptide

<223> Codon biased nucleotide sequence encoding VC1.
 Codon biased for rice.

<400> 12
 atg aac ttc ctc aag tcc ttt ccg ttc tac gcc ttc ctg tgc ttt ggc 48
 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly
 -25 -20 -15 -10
 cag tat ttc gtg gcg gtc acc cac gct gcc tgg atc tcc gag aag aaa 96
 Gln Tyr Phe Val Ala Val Thr His Ala Ala Trp Ile Ser Glu Lys Lys
 -5 1 5
 gtg cag gac gtc att gat aag aag ctc ccg aac ggc atg gtt aag aat 144
 Val Gln Asp Val Ile Asp Lys Lys Leu Pro Asn Gly Met Val Lys Asn
 10 15 20
 gcg ata aaa gct gta gtg cac aag gca gcc aag aac aag cat ggg tgc 192
 Ala Ile Lys Ala Val Val His Lys Ala Ala Lys Asn Lys His Gly Cys
 25 30 35
 ttc gcg gac ttt gat gtc gga ggc ggc tgt gaa caa cac tgc cag aaa 240
 Phe Ala Asp Phe Asp Val Gly Gly Gly Cys Glu Gln His Cys Gln Lys
 40 45 50 55
 acc gag agc aag gct ggg atc tgc cat gga acg aag tgt aag tgc ggc 288
 Thr Glu Ser Lys Ala Gly Ile Cys His Gly Thr Lys Cys Lys Cys Gly
 60 65 70
 atc ccc cgc gcc tac aaa aag tag 312
 Ile Pro Arg Ala Tyr Lys Lys *
 75

<210> 13
 <211> 103
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PR1 signal peptide linked to VC1

<400> 13
 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly
 1 5 10 15
 Gln Tyr Phe Val Ala Val Thr His Ala Ala Trp Ile Ser Glu Lys Lys
 20 25 30

Val Gln Asp Val Ile Asp Lys Lys Leu Pro Asn Gly Met Val Lys Asn
35 40 45
Ala Ile Lys Ala Val Val His Lys Ala Ala Lys Asn Lys His Gly Cys
50 55 60
Phe Ala Asp Phe Asp Val Gly Gly Gly Cys Glu Gln His Cys Gln Lys
65 70 75 80
Thr Glu Ser Lys Ala Gly Ile Cys His Gly Thr Lys Cys Lys Cys Gly
85 90 95
Ile Pro Arg Ala Tyr Lys Lys
100

<210> 14
<211> 240
<212> DNA
<213> Artificial Sequence

<220>
<223> Codon biased nucleotide sequence encoding Aaml.
Codon biased rice.

<221> CDS
<222> (64)...(240)
<221> sig_peptide
<222> (1)...(63)
<223> Sweet potato sporamin signal

<400> 14
atg aag gcc ttc acc ctc gcg ctg ttt ctc gct ctc tcc ttg tat ctt 48
Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu
-20 -15 -10
ctc ccc aac cca gcg gct gac gtc ccg gga aac tac cca ctt gat tct 96
Leu Pro Asn Pro Ala Ala Asp Val Pro Gly Asn Tyr Pro Leu Asp Ser
-5 1 5 10
tcc gac aat acc tac ctg tgc gcc cct ttg gga gat aat ccg gac tgc 144
Ser Asp Asn Thr Tyr Leu Cys Ala Pro Leu Gly Asp Asn Pro Asp Cys
15 20 25
att aag atc tgt cag aaa cac ggt gtg gat tac ggg tat tgc tac gcc 192
Ile Lys Ile Cys Gln Lys His Gly Val Asp Tyr Gly Tyr Cys Tyr Ala
30 35 40
ttc caa tgc tgg tgt gaa ttt ctg aag gat gag aac gtg aag gtc tga 240
Phe Gln Cys Trp Cys Glu Phe Leu Lys Asp Glu Asn Val Lys Val *
45 50 55

<210> 15
<211> 79
<212> PRT
<213> Artificial Sequence

<220>

<221> SIGNAL

<222> (1)...(21)

<223> Codon biased nucleotide sequence encoding Aam1.
Codon biased to rice.

<400> 15

Met	Lys	Ala	Phe	Thr	Leu	Ala	Leu	Phe	Leu	Ala	Leu	Ser	Leu	Tyr	Leu
-20					-15					-10					
Leu	Pro	Asn	Pro	Ala	Ala	Asp	Val	Pro	Gly	Asn	Tyr	Pro	Leu	Asp	Ser
-5				1				5					10		
Ser	Asp	Asn	Thr	Tyr	Leu	Cys	Ala	Pro	Leu	Gly	Asp	Asn	Pro	Asp	Cys
			15				20					25			
Ile	Lys	Ile	Cys	Gln	Lys	His	Gly	Val	Asp	Tyr	Gly	Tyr	Cys	Tyr	Ala
	30						35					40			
Phe	Gln	Cys	Trp	Cys	Glu	Phe	Leu	Lys	Asp	Glu	Asn	Val	Lys	Val	
45					50					55					

<210> 16

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> SPAam1 sporamin signal and Aam1

<221> SIGNAL

<222> (1)...(21)

<400> 16

Met	Lys	Ala	Phe	Thr	Leu	Ala	Leu	Phe	Leu	Ala	Leu	Ser	Leu	Tyr	Leu
-20					-15					-10					
Leu	Pro	Asn	Pro	Ala	Ala	Asp	Val	Pro	Gly	Asn	Tyr	Pro	Leu	Asp	Ser
-5				1				5					10		
Ser	Asp	Asn	Thr	Tyr	Leu	Cys	Ala	Pro	Leu	Gly	Asp	Asn	Pro	Asp	Cys
			15				20					25			
Ile	Lys	Ile	Cys	Gln	Lys	His	Gly	Val	Asp	Tyr	Gly	Tyr	Cys	Tyr	Ala
	30						35					40			
Phe	Gln	Cys	Trp	Cys	Glu	Phe	Leu	Lys	Asp	Glu	Asn	Val	Lys	Val	
45					50					55					

<210> 17

<211> 249

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon biased nucleotide sequence encoding Aam1.
Codon biased to Streptomyces coelicolor.

<221> CDS

<222> (73)...(249)

<221> sig_peptide

<222> (1)...(72)

<223> BAA signal peptide

<400> 17

```

atg gcc aac aag cac ctg tcc ctg tgc tta ttc ctg gtc ctc ctc ggc 48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
      -20                      -15                      -10

ctc tcc gcc tcc ctc gcg agc ggt gcc gac gtg cca ggg aac tac ccg 96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Asp Val Pro Gly Asn Tyr Pro
      -5                      1                      5

ctg gac agc tgc gac aac acc tac ctg tgc gca ccc ctg ggc gac aac 144
Leu Asp Ser Ser Asp Asn Thr Tyr Leu Cys Ala Pro Leu Gly Asp Asn
      10                      15                      20

ccg gac tgc atc aag atc tgc cag aag cac ggc gtc gac tac ggc tac 192
Pro Asp Cys Ile Lys Ile Cys Gln Lys His Gly Val Asp Tyr Gly Tyr
      25                      30                      35                      40

tgc tac gcg ttc cag tgt tgg tgc gag ttc ctg aag gac gag aac gtc 240
Cys Tyr Ala Phe Gln Cys Trp Cys Glu Phe Leu Lys Asp Glu Asn Val
      45                      50                      55

aag gtg tga 249
Lys Val *
```

<210> 18

<211> 82

<212> PRT

<213> Artificial Sequence

<220>

<221> SIGNAL

<222> (1)...(24)

<223> Codon biased nucleotide sequence encoding Aam1.
Codon biased to Streptomyces coelicolor.

<400> 18

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
      -20                      -15                      -10

Leu Ser Ala Ser Leu Ala Ser Gly Ala Asp Val Pro Gly Asn Tyr Pro
      -5                      1                      5

Leu Asp Ser Ser Asp Asn Thr Tyr Leu Cys Ala Pro Leu Gly Asp Asn
      10                      15                      20

Pro Asp Cys Ile Lys Ile Cys Gln Lys His Gly Val Asp Tyr Gly Tyr
      25                      30                      35                      40

Cys Tyr Ala Phe Gln Cys Trp Cys Glu Phe Leu Lys Asp Glu Asn Val
      45                      50                      55

Lys Val
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<210> 19

<211> 82

<400> 21
ggccgctcta gaactagtgg atccccggg ctgcaggaat tcggcacgag acattttacc 60
ataacggtaa aaacgtttct attaatactt tcttttagtga aaaaaaactt gaaagt atg 119
Met
1

aaa ttc ttc cta att gtg tca ttg gca ata atg tcg tgt ttc atg gaa 167
Lys Phe Phe Leu Ile Val Ser Leu Ala Ile Met Ser Cys Phe Met Glu
5 10 15

atg aaa gaa gta tac gca ggt acg aaa gga aat ttt ccc gtc gat ttt 215
Met Lys Glu Val Tyr Ala Gly Thr Lys Gly Asn Phe Pro Val Asp Phe
20 25 30

caa gga ata ttt tac gaa tgc atc gta tac aat aga tgt gaa cgc gac 263
Gln Gly Ile Phe Tyr Glu Cys Ile Val Tyr Asn Arg Cys Glu Arg Asp
35 40 45

tgc aag tta cat gga tcg agt tat ggc tat tgc tac gct gga gtt tgc 311
Cys Lys Leu His Gly Ser Ser Tyr Gly Tyr Cys Tyr Ala Gly Val Cys
50 55 60 65

tac tgc gaa ggt tta gct gac gaa gat aaa tat ttc ctg gga atg taa 359
Tyr Cys Glu Gly Leu Ala Asp Glu Asp Lys Tyr Phe Leu Gly Met *
70 75 80

tgaaaaaaca atgccgatta aatgtaaaat caatatcggt attgccctac aataagcgat 419
taatcntttt gngagattaa ccttggaat aatggttacc taaaaaactn gggaataaaa 479

<210> 22
<211> 80
<212> PRT
<213> Centruroides vittatus

<400> 22
Met Lys Phe Phe Leu Ile Val Ser Leu Ala Ile Met Ser Cys Phe Met
1 5 10 15
Glu Met Lys Glu Val Tyr Ala Gly Thr Lys Gly Asn Phe Pro Val Asp
20 25 30
Phe Gln Gly Ile Phe Tyr Glu Cys Ile Val Tyr Asn Arg Cys Glu Arg
35 40 45
Asp Cys Lys Leu His Gly Ser Ser Tyr Gly Tyr Cys Tyr Ala Gly Val
50 55 60
Cys Tyr Cys Glu Gly Leu Ala Asp Glu Asp Lys Tyr Phe Leu Gly Met
65 70 75 80

<210> 23
<211> 243
<212> DNA
<213> Centruriodes vittatus

<400> 23
atgaaattct tcctaattgt gtcattggca ataatgtcgt gtttcatgga aatgaaagaa 60
gtatacgag gtacgaaagg aaattttccc gtcgattttc aaggaaatatt ttacgaaatgc 120

atcgataaca atagatgtga acgcgactgc aagttacatg gatcgagtta tggctattgc 180
 tacgctggag tttgctactg cgaagggtta gctgacgaag ataaatattt cctgggaatg 240
 taa 243

<210> 24

<211> 57

<212> PRT

<213> *Centruroides vittatus*

<400> 24

Gly	Thr	Lys	Gly	Asn	Phe	Pro	Val	Asp	Phe	Gln	Gly	Ile	Phe	Tyr	Glu
1				5				10					15		
Cys	Ile	Val	Tyr	Asn	Arg	Cys	Glu	Arg	Asp	Cys	Lys	Leu	His	Gly	Ser
		20					25					30			
Ser	Tyr	Gly	Tyr	Cys	Tyr	Ala	Gly	Val	Cys	Tyr	Cys	Glu	Gly	Leu	Ala
	35					40						45			
Asp	Glu	Asp	Lys	Tyr	Phe	Leu	Gly	Met							
50						55									

<210> 25

<211> 292

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon biased nucleotide sequence encoding Ts7.
 Codon biased to *Streptomyces coelicolor*.

<221> CDS

<222> (73)...(292)

<221> sig_peptide

<222> (1)...(72)

<223> BAA signal sequence

<400> 25

atg	gcg	aac	aag	cac	ctc	tcc	ctg	tcg	ctg	ttc	ctc	gtc	ctg	ctg	ggc	48
Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly	
				-20					-15				-10			
ctg	tcg	gcg	agc	ctc	gcc	tcc	ggc	ggg	acc	aag	ggc	aac	ttc	ccg	gtc	96
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Gly	Thr	Lys	Gly	Asn	Phe	Pro	Val	
			-5				1				5					
gac	ttc	cag	ggc	atc	ttc	tac	gag	tgc	atc	gtg	tac	aac	cgc	tgc	gag	144
Asp	Phe	Gln	Gly	Ile	Phe	Tyr	Glu	Cys	Ile	Val	Tyr	Asn	Arg	Cys	Glu	
	10				15					20						
cgg	gac	tgt	aag	ctg	cac	ggc	agc	tcc	tac	ggc	tac	tgc	tac	gcc	ggc	192
Arg	Asp	Cys	Lys	Leu	His	Gly	Ser	Ser	Tyr	Gly	Tyr	Cys	Tyr	Ala	Gly	
	25				30				35					40		
gtg	tgc	tac	tgc	gag	ggg	ctc	gcc	gac	gaa	gac	aag	tac	ttc	ctg	gga	240
Val	Cys	Tyr	Cys	Glu	Gly	Leu	Ala	Asp	Glu	Asp	Lys	Tyr	Phe	Leu	Gly	
			45					50						55		

atg taa gac gct ccc cga gcg gct gct tct gtt cat gaa gga ccc tta 288
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cat t 292
 His

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 -5 1 5
 Asp Phe Gln Gly Ile Phe Tyr Glu Cys Ile Val Tyr Asn Arg Cys Glu
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 Arg Asp Cys Lys Leu His Gly Ser Ser Tyr Gly Tyr Cys Tyr Ala Gly
 25 30 35 40
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 Met

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<400> 27
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 20 25 30
 Ser Gly Tyr Cys Gln Trp Phe Gly Arg Tyr Gly Asn Ala Cys Trp Cys
 35 40 45
 Ile Lys Leu Pro Asp Lys Val Pro Ile Lys Val Pro Gly Lys Cys Asn
 50 55 60